

IN THE CLAIMS

1-3. (canceled) .

4. (currently amended)      A method for reducing sequencing errors by sequencing, recovering and resequencing a single-stranded template nucleic acid, the method comprising:

- (a)    forming an array of immobilised single-stranded template nucleic acid molecules wherein the density of immobilised single-stranded template nucleic acid molecules is  $10^6$ - $10^9$  different template sequences per  $\text{cm}^2$   
~~covalently attaching a single-stranded template nucleic acid to the 5' end of a hairpin nucleic acid, wherein the hairpin nucleic acid is self-complementary and has a first restriction site for a nicking endonuclease, said restriction site comprising a recognition sequence and a cleavage site, wherein said recognition sequence is situated so that said cleavage site is before, at, or beyond the 3' end of the hairpin nucleic acid, and wherein said hairpin nucleic acid is a self-hybrid;~~
- (b)    determining the sequences of the immobilised single-stranded template nucleic acid molecules by synthesising a complementary copy of the template sequences, thereby performing a first round of sequencing  
~~sequencing a first portion of the single-stranded template nucleic acid by using the 3' end of the hairpin nucleic acid as a primer and extending said primer to generate a nucleic acid strand complementary to the first portion of the single-stranded template nucleic acid, thereby generating a hairpin-template-complement nucleic acid complex, wherein the template and its complementary strand are covalently attached;~~
- (c)    removing the complementary synthetic strand; and contacting the hairpin-template-complement nucleic acid complex with said nicking endonuclease, under conditions where the nicking endonuclease cleaves

~~before, at or beyond the 3' end of the hairpin nucleic acid, thereby providing a nicked hairpin-template-complement nucleic acid complex;~~

(d) performing a second round of sequencing of the immobilised single-stranded template nucleic acid molecules, wherein comparison of first and second rounds of sequencing of each immobilized single-stranded template nucleic acid molecule reduces sequencing errors ~~subjecting the nicked hairpin-template-complement nucleic acid complex to conditions whereby the nucleic acid strand complementary to the template nucleic acid dissociates from the template nucleic acid,~~

~~—thereby removing the nucleic acid strand complementary to said first portion of the single-stranded template nucleic acid and recovering the single-stranded template nucleic acid; and~~

(e) ~~—resequencing the first portion of the single-stranded template nucleic acid by using the 3' end of the hairpin nucleic acid as a primer and extending said primer to generate a second nucleic acid strand complementary to said first portion of the single-stranded template nucleic acid, wherein the template and the second complementary strand are covalently attached.~~

5-26. (canceled).

27. (new)      The method of claim 4, wherein the template polynucleotides are attached to a double stranded anchor.

28 (new)      The method of claim 28, wherein the double stranded anchor comprises a self complementary hairpin.

29 (new)      The method of claim 27, wherein the double stranded anchor comprises a

recognition site for a restriction endonuclease.

30 (new)      The method of claim 4, wherein the  $10^6$ - $10^9$  templates are individually resolvable single molecules.

31 (new)      The method of claim 4, wherein the sequencing determination is carried out using cycles of incorporation and detection of fluorescently labeled nucleotides.

32 (new)      The method of claim 31, wherein the fluorescent nucleotides are detected using a microscope with total internal reflection based imaging.